Phylogeography and connectivity of four sibling species of *Pseudocalanus* (Copepoda: Calanoida) in the North Pacific and Arctic Ocean

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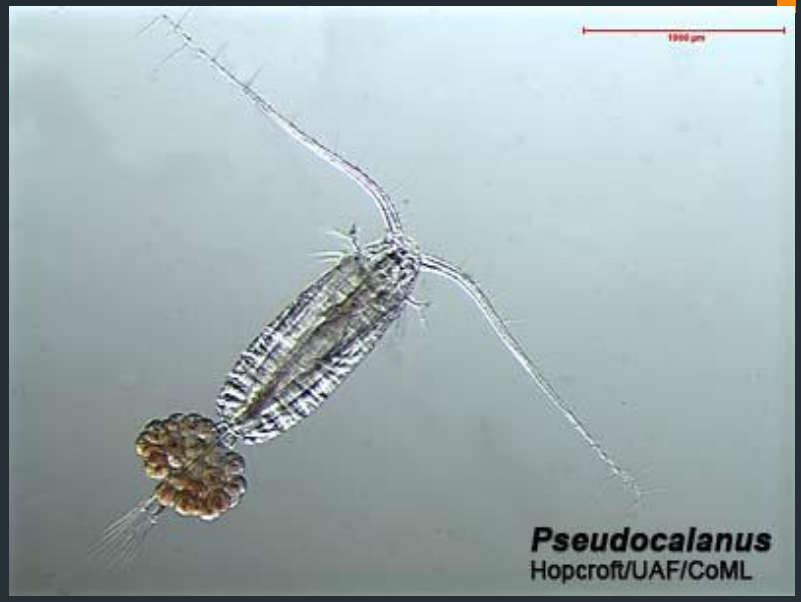
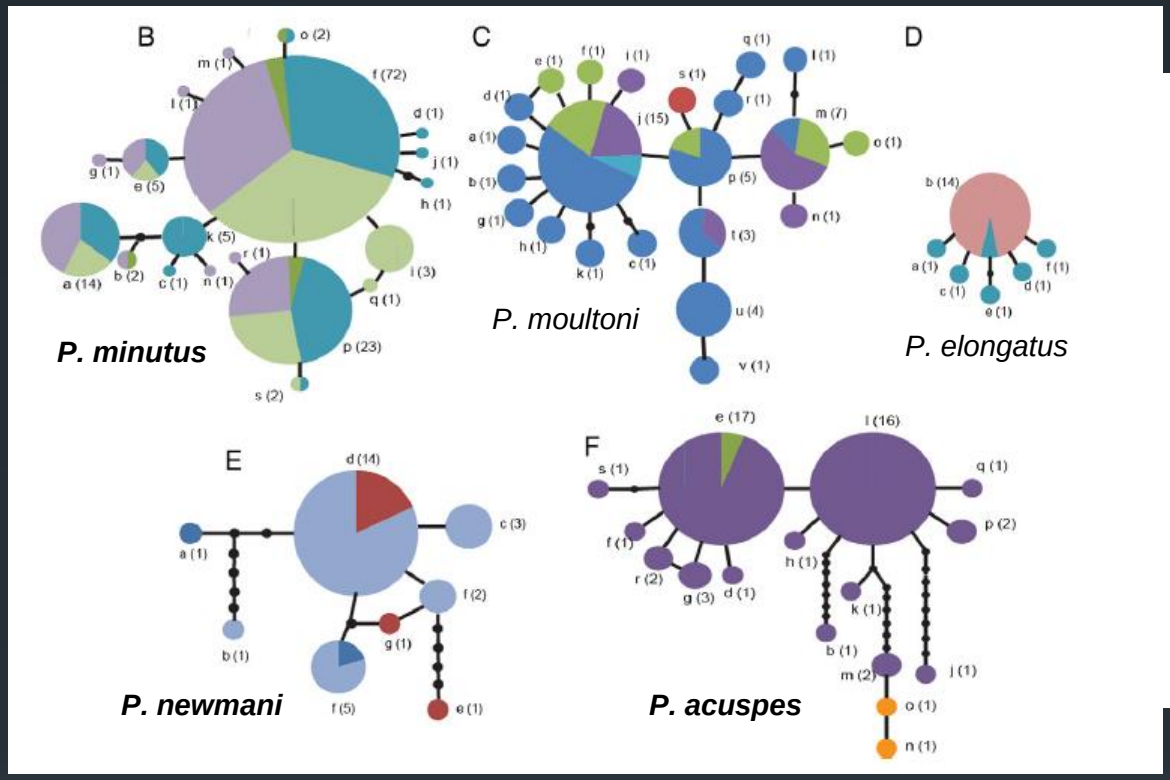
Statoil ConocoPhillips Olgoonik Fairweather LLC

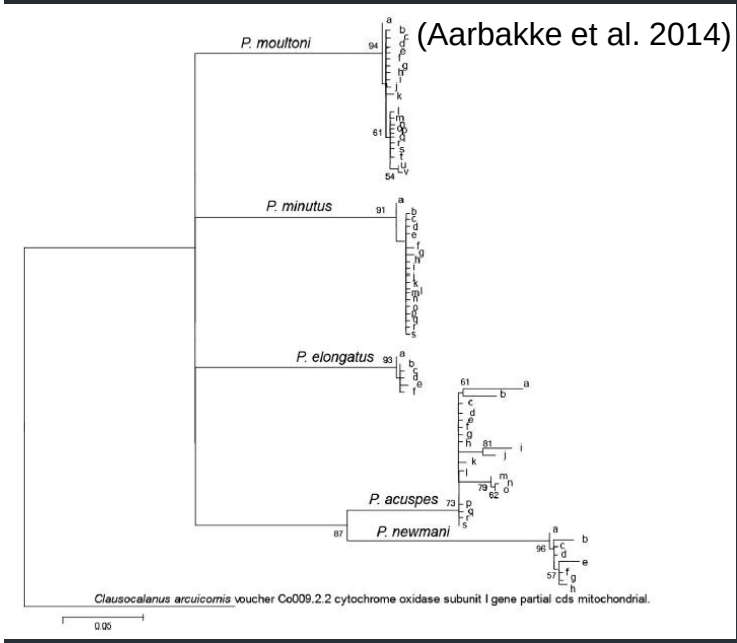
Pseudocalanus spp.



- Calanoid copepod – 7 species total
- Habitat preference
  - Arctic/subarctic species
    - Arctic: *P. acuspes* and *P. minutus*
    - Temperate: *P. newmani* and *P. mimus*
  - all 4 species occur sympatrically
- Numerically dominant in North Pacific and Western Arctic
  - GAK/PWS (Coyle & Pinchuk, 2005)
  - Bering Sea (Coyle et al, 2008)
  - Chukchi Sea (Hopcroft et al, 2010; Questel et al, 2013) ~33% of holozooplankton community
  - Beaufort Sea (Smoot & Hopcroft, in prep) ~50% of copepod abundance
- Important food web component
- Taxonomic difficulties

Previous *Pseudocalanus* COI work





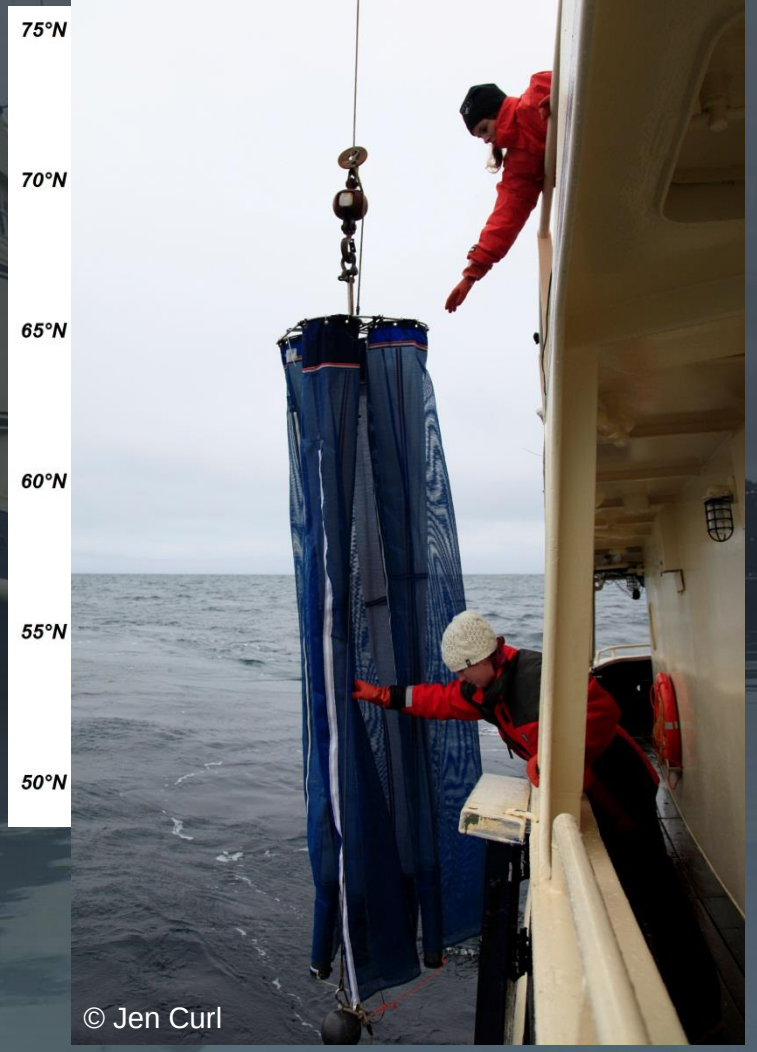
- Aarbakke et al. (2014): COI, CytB, and ITS-1 for phylogeography and demographic history analysis
  - ***P. acuspes, P. newmani, P. minutus***, *P. moultoni,* and *P. elongatus*
  - suggests two diverging evolutionary branches
- No published COI work for the North Pacific or Western Arctic

Study design

- mtCOI sequencing from:
- GoA & PWS glacial fjords
  - Seward Line Research Program
- Chukchi
  - CSESP (Chukchi Sea Environmental Studies Program)
- Beaufort
  - Transboundary Project

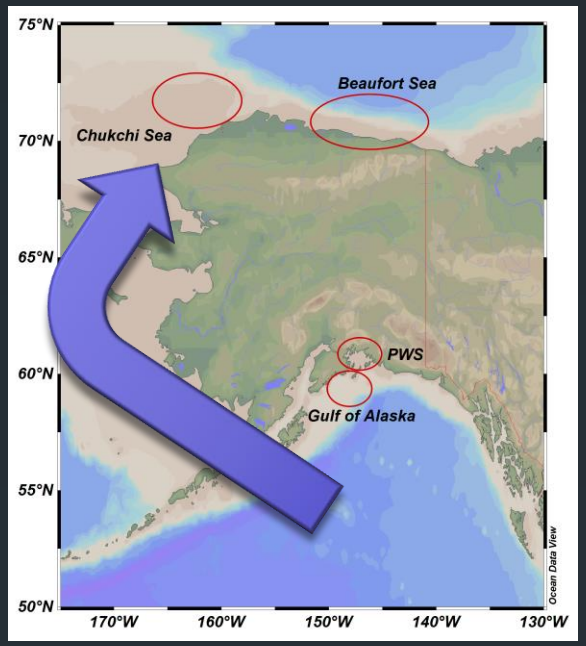
- All samples collected during the 2013 field season
- Collection via 150 μm-mesh net
- Preserved in 190-proof ethanol

Desi n



Objectives

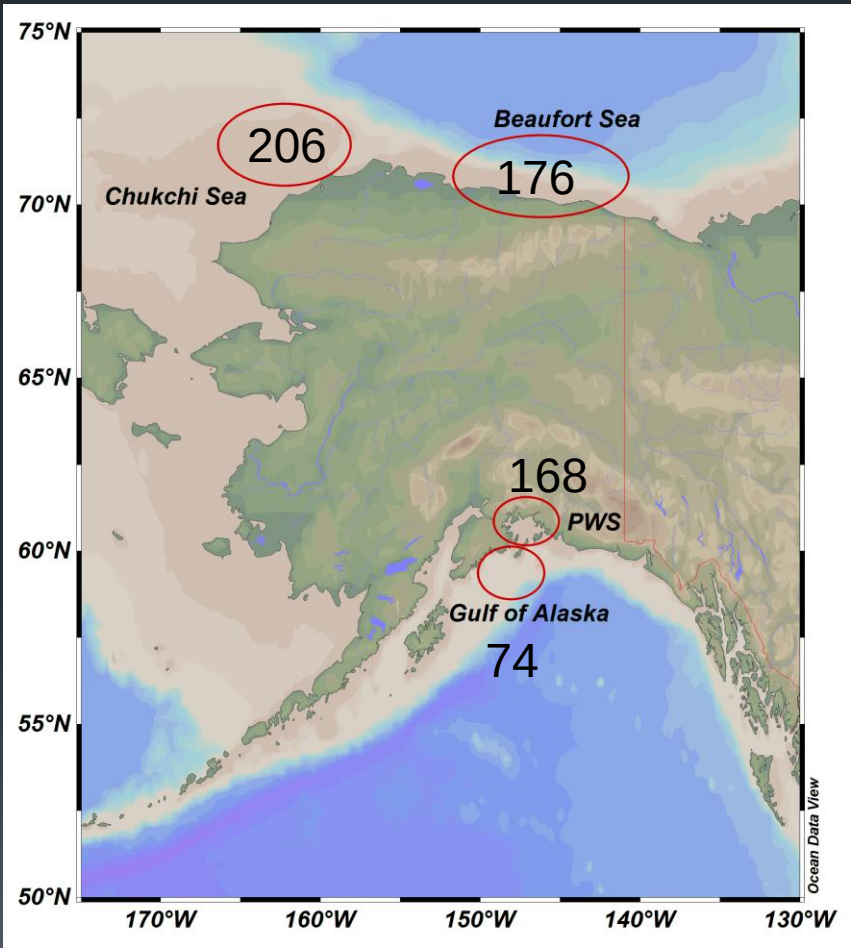
- To determine the degree of population connectivity (gene flow) between the North Pacific and Western Arctic Ocean for 4 sibling species of *Pseudocalanus* using mitochondrial DNA
- Characterize population structure of *Pseudocalanus* spp.



Results

- 624 *Pseudocalanus* have been sequenced to date
  - Still filling in gaps

Region	*P. acuspes*	*P. minutus*	*P. newmani*	*P. mimus*	Total
Columbia Glacier	1	3	36	37	**77**
Icy Bay	0	16	60	15	**91**
GoA	1	0	39	34	**74**
Chukchi Sea	139	28	37	2	**206**
Beaufort Sea	80	49	35	2	**176**



Population comparison

F_{ST} distances

- Measure of population differentiation due to genetic structure
- 0 – 1 range: lower the F_{ST} value the higher the gene flow

P. mimus and *P. newmani* (Temperate)

P. mimus	Beaufort	Chukchi Sea	Columbia Glacier	Icy Bay	Gulf of Alaska
Beaufort	–				
Chukchi Sea	0.0329	–			
Columbia Glacier	**0.33629***	-0.14918	–		
Icy Bay	**0.32928***	-0.18557	0.01633	–	
Gulf of Alaska	**0.35623***	-0.08704	0.00756	0.01998	–
P. newmani					
Beaufort	–				
Chukchi Sea	**0.20185***	–			
Columbia Glacier	**0.17982***	-0.00958	–		
Icy Bay	**0.30906***	0.01269	0.01726	–	
Gulf of Alaska	**0.32190***	0.01449	0.02226	0.00964	–

Population comparison

F_{ST} distances

- Measure of population differentiation due to genetic structure
- 0 – 1 range: lower the F_{ST} value the higher the gene flow

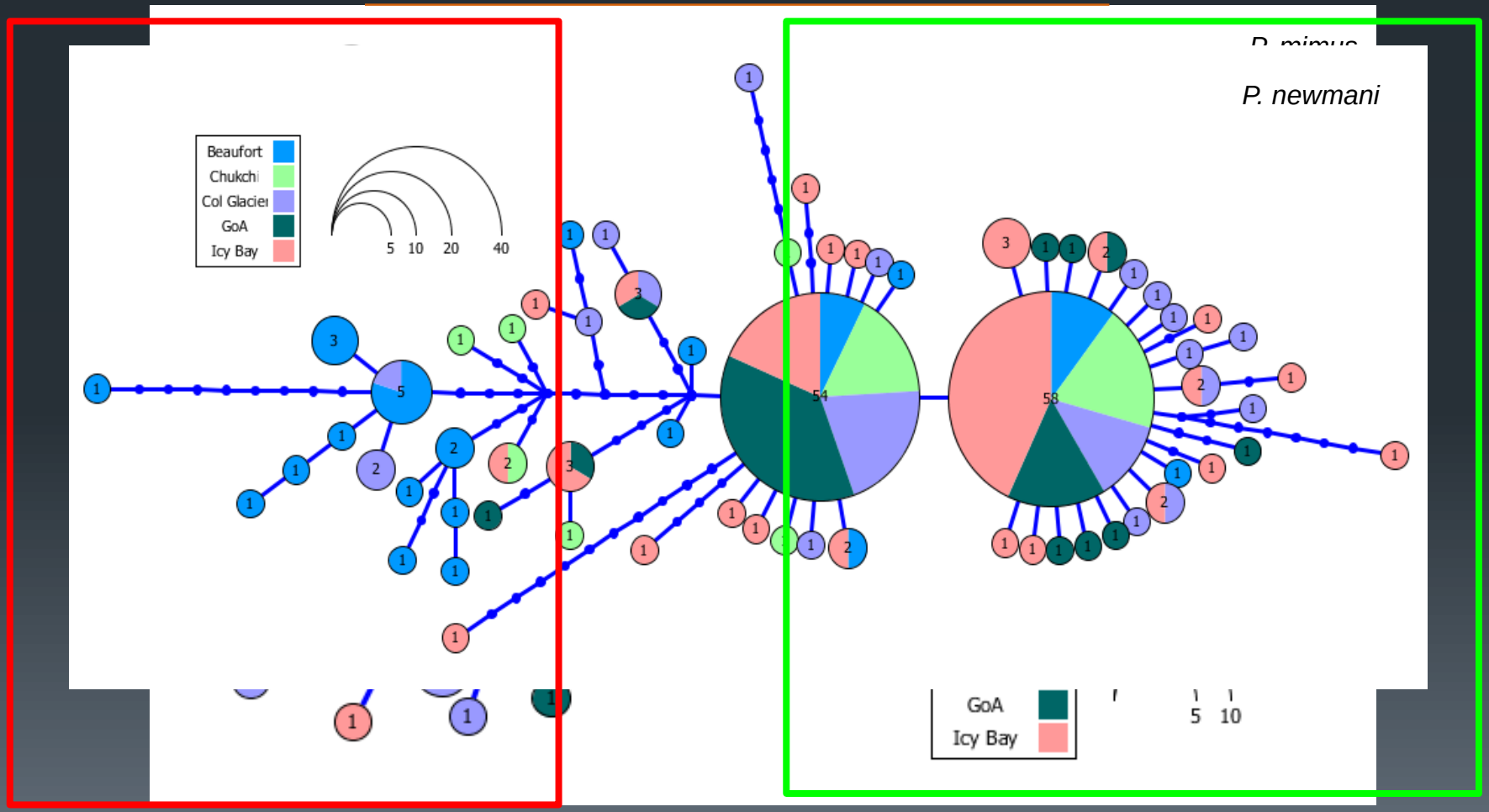
P. acuspes and *P. minutus* (Arctic)

P. acuspes	Beaufort	Chukchi Sea	Columbia Glacier	Gulf of Alaska
Beaufort	–			
Chukchi Sea	**0.08620***	–		
Columbia Glacier	-0.71771	-0.96088	–	
Gulf of Alaska	0.51802	0.83288	1.00000	–

P. minutus	Beaufort	Chukchi Sea	Columbia Glacier	Icy Bay
Beaufort	–			
Chukchi Sea	-0.00592	–		
Columbia Glacier	0.11672	0.14376	–	
Icy Bay	0.04485	0.02918	0.11543	–

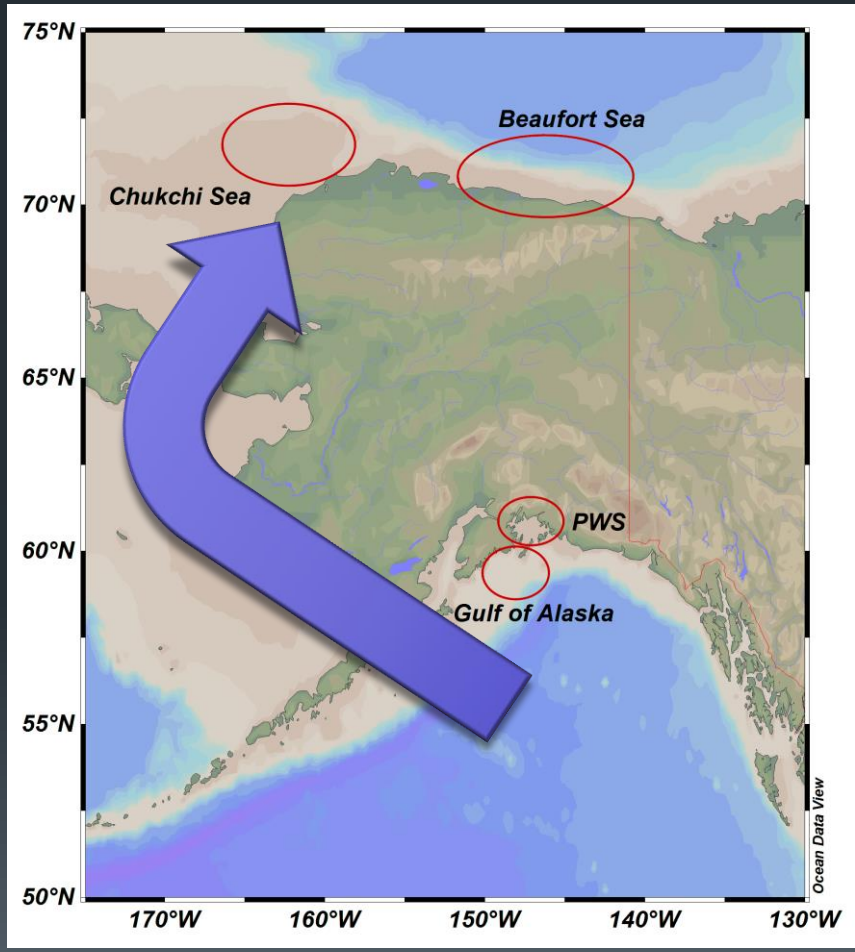
Haplotype Networks

	P. acuspes	*P. minutus*	*P. mimus*	*P. newmani*
# Haplotypes	53	20	61	70
Hd	0.652	0.677	0.954	0.849



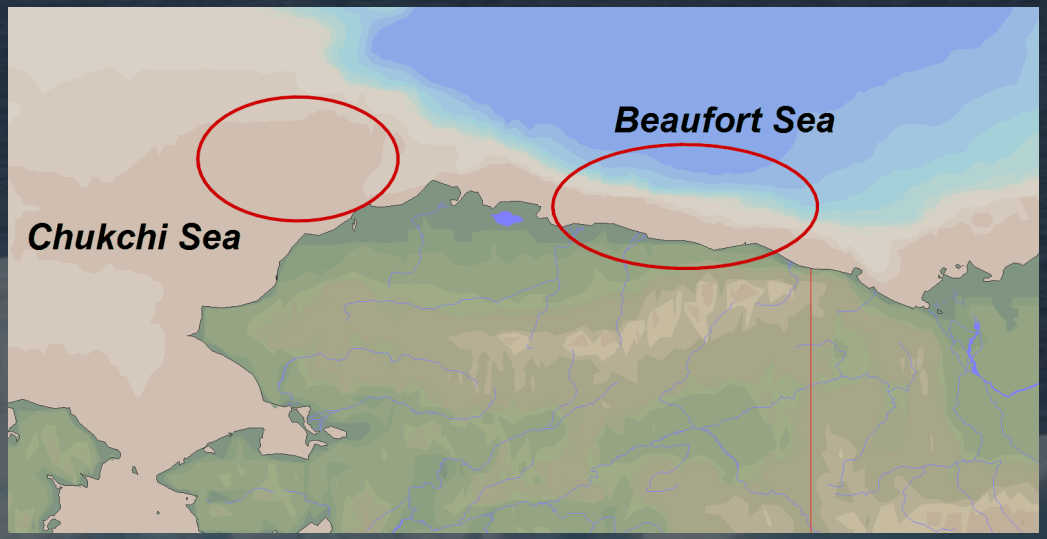
Population connectivity

- Migrate-n estimates migration rates and effective population size using genetic data
- Allows for asymmetrical migration rates at different subpopulation sizes
- Another use: compare migrate model probabilities through Bayes Factors - ratios of marginal likelihoods (Beerli & Palczewski, 2010)
- Decide models to compare *a priority,* based on hydrography and geography (not all scenarios are possible!)



Population connectivity

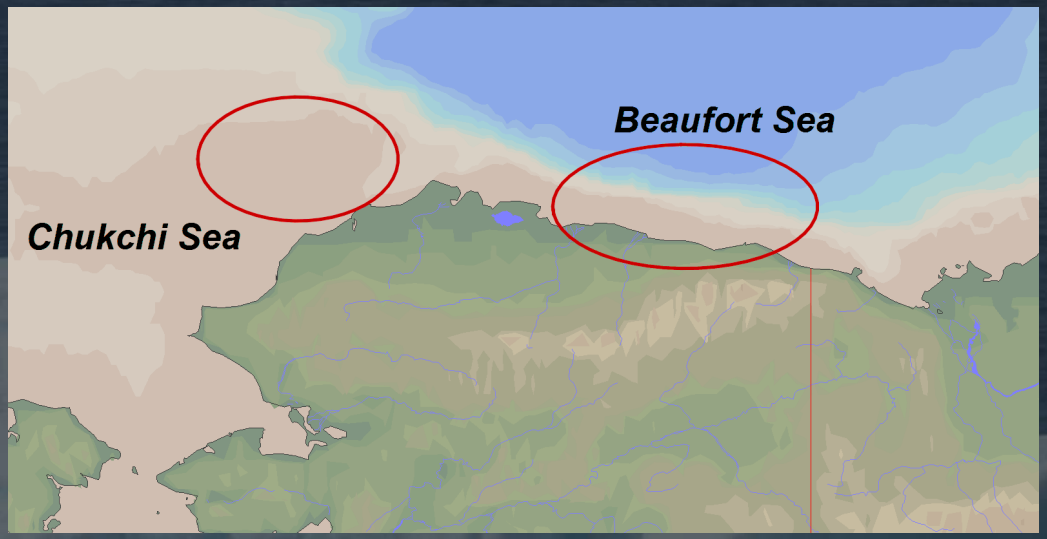
P. acuspes (Arctic)



	CS↔BS	CS→BS	CS←BS
	Full	S to N	N to S
Bezier lLm	-1624.50	-1644.97	-1960.81
Model Probability	1	≈0	≈0
Choice	**1**	**2**	3

Population connectivity

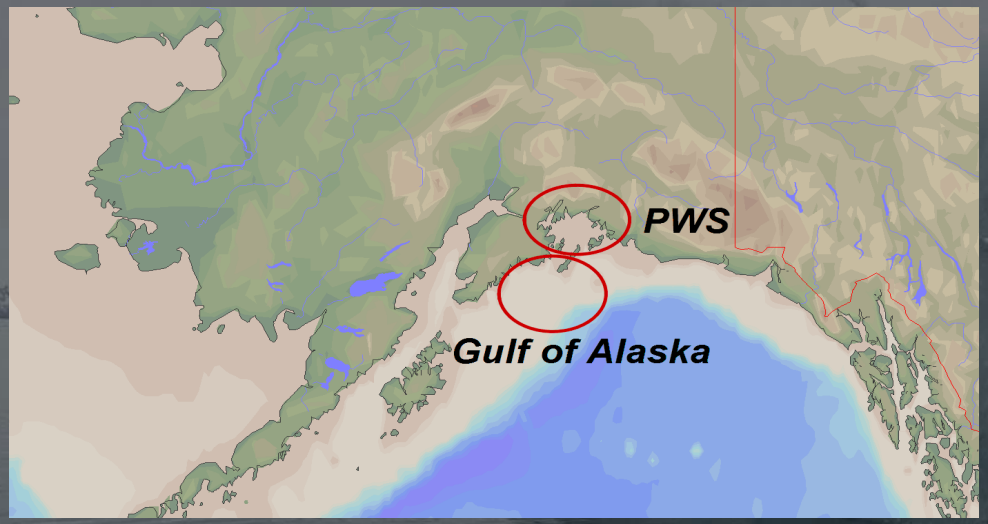
P. minutus (Arctic)

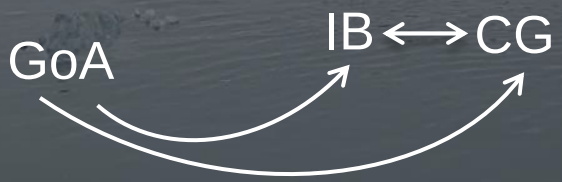


	CS↔BS	CS→BS	CS←BS
	Full	S to N	N to S
Bezier lLm	-973.53	-1283.55	-1278.39
Model Probability	1	≈0	≈0
Choice	**1**	3	2

Population connectivity

P. mimus (Temperate)

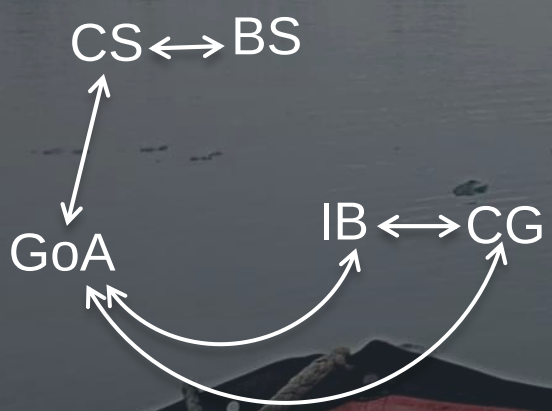


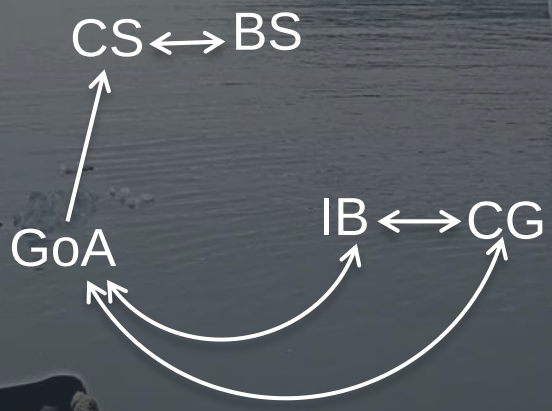


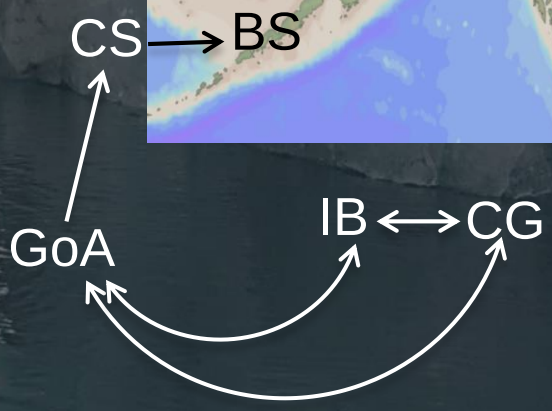
	Full	In	Out
Bezier lLm	-1445.07	-1718.41	-1493.43
Model Probability	1	≈0	≈0
Choice	**1**	3	**2**

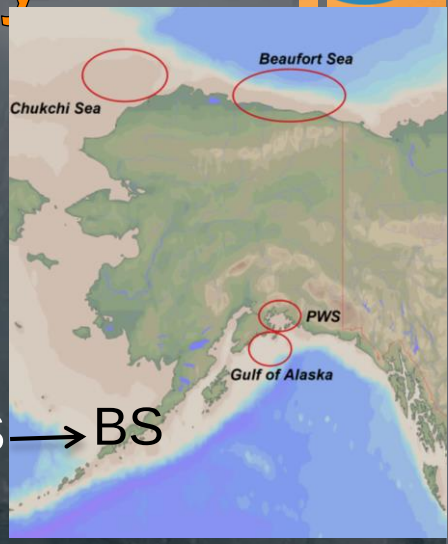
Population connectivity

P. newmani (Temperate)









	Full	North of Bering	All North
Bezier lLm	-2002.72	-1999.19	-2000.32
Model Probability	0.001	0.904	0.095
Choice	3	**1**	2

Summary

- All four *Pseudocalanus* species identified via COI sequencing in all study areas
- Haplotype diversity highest in Temperate species: *P. mimus and P. newmani*
- Haplotype diversity lowest in Arctic species: *P. acuspes* and *P. minutus*
- Connection between Chukchi and Beaufort, and between PWS fjords and the GoA
- Large degree of northward gene flow across the Bering Sea and into the Chukchi Sea

Acknowledgments

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  - ConocoPhillips – Caryn Rea
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Questions?